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H 3 C
SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA GRODEN
- (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
- (iii) NUMBER OF SEQUENCES: 78
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
(B) STREET: 90 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: U.S.A.
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/559,303
(B) FILING DATE: NOVEMBER 15, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: ELIZABETH A. BOGOSIAN
(B) REGISTRATION NUMBER: 39,911
(C) REFERENCE/DOCKET NUMBER: 63475/65
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 697-5995
(B) TELEFAX: (212) 286-0854 or 286-0082
(C) TELEX: TWX 710-581-4766
- (2) INFORMATION FOR SEQ ID NO: 1
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
(A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
GGTGGCGACG ACTCCTGGA 19

(3) INFORMATION FOR SEQ ID NO: 2

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
(A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
ACCAGACCAA CTGGTAATG 19

(4) INFORMATION FOR SEQ ID NO: 3

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
(A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

ATGGTAGCGA CCGGCGCTCA 20

(5) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

CCGTCAGTAT CGGCGGAATT 20

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

TTGTGGTGTT GGGTAGAGGT T 21

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GCCGCCGGCA CCAAC 15

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CCTCAGTCAA ATCTATNTGC TC 22

(9) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

GCCATCACCG GAACAGAAAGG AAA 23

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

TCTTCTGGAG GAGGTGGAAC AA 22

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

GGATCCTGGT TCCGTCCGC 19

(12) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

CAACTAGAAC GTCACTCAGC C 21

(13) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

GACTTTCCCT TCAGTGAAACC TC 22

(14) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

CCAGATTCT TGCAGACTCC G 21

(15) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

CTTAAAGTAC CATCAATGAT TGGG 24

(16) INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

- (C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

GAGTAAGCAC TGCTCAGAAA TC 22

(17) INFORMATION FOR SEQ ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

CGAGCAAATA GATTTGACTG AGG 23

(18) INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:

- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

GAAGATGCTC AGGAAAGTGA C 21

(19) INFORMATION FOR SEQ ID NO: 18

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

CAACTGAGAA AGTTCCATGT ATTG 24

(20) INFORMATION FOR SEQ ID NO: 19

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CTATTCCTGA TGATAAACTG AAAC 24

(21) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GTGGAGATAc AGGCCTGATT C 21

(22) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

CAGGATTCTC TGCCACCAGG 20

(23) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

CAGGAAATGT TCTCACAAAGC AC 22

(24) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

CAGCCAGCAA ATCTTCCACA G 21

(25) INFORMATION FOR SEQ ID NO: 24

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

GAATTATACT GACAAGTCAG CAC 23

(26) INFORMATION FOR SEQ ID NO: 25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CTCCTGGGGT CACTGTTGTC 20

(27) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

GAGGTTCACT GAAGGAAAAG TC 22

(28) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

GAAGTCCTTG ACCCTTGCT G 21

(29) INFORMATION FOR SEQ ID NO: 28

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

GGGATTTCTT TACAGTTGGT GTG 23

(30) INFORMATION FOR SEQ ID NO: 29

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

CTCTTACAAA GTGACTTTGG GG 22

(31) INFORMATION FOR SEQ ID NO: 30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

CCTCAGTCAA ATCTATTG C TCG 23

(32) INFORMATION FOR SEQ ID NO: 31

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

GCTTAACCAT TCTGAGTCAT CC 22

(33) INFORMATION FOR SEQ ID NO: 32

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32
CAATACATGG AACTTTCTCA GTTG 24

(34) INFORMATION FOR SEQ ID NO: 33

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33
CGTACTAAGG CATTGTGAAG AGG 23

(35) INFORMATION FOR SEQ ID NO: 34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

CACAGTCTGT GCTGGTTCT G 21

(36) INFORMATION FOR SEQ ID NO: 35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

CCTTCATAGA ATTCCCTGTA GG 22

(37) INFORMATION FOR SEQ ID NO: 36

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

GTGTTTCAGC CCAGTTGCTA C 21

(38) INFORMATION FOR SEQ ID NO: 37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

GCAGTATGTT TATTCTGATC TTTC 24

(39) INFORMATION FOR SEQ ID NO: 38

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

CCTTGATGGG TTGATAGGCA G 21

(40) INFORMATION FOR SEQ ID NO: 39

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

CGCTCATGTT TCAGATTCT GG 22

(41) INFORMATION FOR SEQ ID NO: 40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

GATCTACGAT AAGTGATCTC AAG 23

(42) INFORMATION FOR SEQ ID NO: 41

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

GAGTCTGTTA CTTGCACAGA TC 22

(43) INFORMATION FOR SEQ ID NO: 42

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

CAATCATAAA ACTTCTATAT GTCAC 25

(44) INFORMATION FOR SEQ ID NO: 43

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

GTGGGGACAT GATTTTCGTC AAG 23

(45) INFORMATION FOR SEQ ID NO: 44

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

GACATCCTGA CTCAGCTGAA G 21

(46) INFORMATION FOR SEQ ID NO: 45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

GCACCACCCA TATGATTCA G 21

(47) INFORMATION FOR SEQ ID NO: 46

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

GATGAAGTGC AGCAGAAGTG G 21

(48) INFORMATION FOR SEQ ID NO: 47

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

GCAGAGCTGG AAGAGATGGG 20

(49) INFORMATION FOR SEQ ID NO: 48

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

GTATAGCATG GTACATTACT GTG 23

(50) INFORMATION FOR SEQ ID NO: 49

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

GACTGACCGAT GTGAAAAGTA TTG 23

(51) INFORMATION FOR SEQ ID NO: 50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

CCAGTCAGGT ATATTTGGAA AAG 23

(52) INFORMATION FOR SEQ ID NO: 51

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

CGATCGCTTA TGTGATGCTC G 21

(53) INFORMATION FOR SEQ ID NO: 52

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

GAACTTACAG AAGTCTGCAA ATC 23

(54) INFORMATION FOR SEQ ID NO: 53

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

GGTGTTACTG AAGACAACT GG 22

(55) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

GGATAAGCCT GTCCAGCAGC 20

(56) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

GCTTCCAGTG GTTCCAAGGC 20

(57) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

CTCAAGCGAC ATCAGGAGCC 20

(58) INFORMATION FOR SEQ ID NO: 57

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

GCCATCACCG GAACAGAAGG 20

(59) INFORMATION FOR SEQ ID NO: 58

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

GATTATGTCT GTTAAAGCTC ATG 23

(60) INFORMATION FOR SEQ ID NO: 59

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

CGTGTCAAGCC ATGGTGTCAC 20

(61) INFORMATION FOR SEQ ID NO: 60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

CAGATAACCT GACAGCCATC C 21

(62) INFORMATION FOR SEQ ID NO: 61

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

CAGTCTGGTC ACATCATGAT AG 22

(63) INFORMATION FOR SEQ ID NO: 62

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

GCTGTATTCT CCTGCATTCC G 21

(64) INFORMATION FOR SEQ ID NO: 63

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

CCTTGTGATG AACTATGTTC TTG 23

(65) INFORMATION FOR SEQ ID NO: 64

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

CCAAAATCTT GTCAAGTATC AGC 23

(66) INFORMATION FOR SEQ ID NO: 65

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

GGAATTTCT GTTTCCATAA AGTC 24

(67) INFORMATION FOR SEQ ID NO: 66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

CAAGCTTCTT GAGAGTGACG G 21

(68) INFORMATION FOR SEQ ID NO: 67

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

GATGTCCATT CAGAGTATTT CTG 23

(69) INFORMATION FOR SEQ ID NO: 68

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

GGGTATTCC TCGTCAAGCT C 21

(70) INFORMATION FOR SEQ ID NO: 69

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

CCTAGATATC TTTCTACATG TGG 23

(71) INFORMATION FOR SEQ ID NO: 70

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

GTTATGAGAA TGCATATGAA GGC 23

(72) INFORMATION FOR SEQ ID NO: 71

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

CAAGAATAAAC AGCTTTATAG TCAC 24

(73) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4437
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

GC	CG	GG	CG	GC	CGTGGTTGCG	GCGCGGGAAG	TTTGGATCCT	GGTCCGTCC	GCTAGGAGTC	60
TG	CG	TG	CAG	GATTATGGCT	GCTGTCCTC	AAAATAATCT	ACAGGAGCAA	CTAGAACGTC		120
A	CT	CAG	CC	AG	AACACTTAAT	AATAAAATTAA	GTCTTCAAA	ACCAAAATT	TCAGGTTCA	180
C	TT	TT	AA	AA	CTTTAAAAAA	GAAAACATCT	TCAGATAACA	ATGTATCTGT	AACTAATGTG	240
A	AA	AC	CT	GT	AAACACCTGT	ATTAAGAAAT	AAAGATGTTA	ATGTTACCGA	AGACTTTCC	300
C	CT	TAC	CC	AA	CTCTACCCAA	CACCACAAAT	CAGCAAAGGG	TCAAGGACTT	TTCAAGTGAAC	360
G	AC	AG	AA	AC	GACAGGAAAC	ACAGAGAGGT	GGATCAAAT	CATTATTGCC	AGATTCTTG	420
A	GG	AG	TT	GT	AGGAAGTTGT	ATGCACTACC	CAAAACACAC	CAACTGTAAA	GAAATCCC GG	480
T	CA	AA	TT	AG	TCAAGAAATT	AGAATTTAGT	TCTTCACCAAG	ATTCTTAAG	TACCATCAAT	540
A	AT	GG	AT	GA	ATATGGATGA	CTTGATACT	TCTGAGACTT	CAAAATCATT	TGTTACACCA	600
C	TT	AA	TA	AG	ACTTTGTAAG	AGTAAGCACT	GCTCAGAAAT	CAAAAAAGGG	TAAGAGAAAC	660
A	AC	AC	AA	AC	CACAGCTTTA	TACAACAAAC	ACAGTAAAGA	CTGATTTGCC	TCCACCCCTCC	720
G	AA	AT	AG	GA	AGCAAATAGA	TTTGACTGAG	GAACAGAAGG	ATGACTCAGA	ATGGTTAAGC	780
T	TC	CAT	CG	GA	TTTGCATCGA	TGATGGCCCC	ATTGCTGAAG	TGCATATAAA	TGAAGATGCT	840
A	CT	CT	GT	AA	ACTCTCTGAA	AACTCATTG	GAAGATGAAA	GAGATAATAG	CGAAAAGAAG	900

AAGAAGCTGA ATTACATTCA ACTGAGAAAG TTCCATGTAT TGAATTTGAT GATGATGATT 960
ATGATAACGGA TTTTGTCCA CCTTCTCCAG AAGAAATTAT TTCTGCTTCT TCTTCCTCTT 1020
CAAAATGCCT TACTACGTTA AAGGACCTTG ACACATCTGA CAGAAAAGAG GATGTTCTTA 1080
GCACATCAAA AGATCTTTG TCAAAAACCTG AGAAAATGAG TATGCAGGAG CTGAATCCAG 1140
AAACCAGCAC AGACTGTGAC GCTAGACAGA TAAGTTACA GCAGCAGCTT ATTCATGTGA 1200
TGGAGCACAT CTGTAAATTA ATTGATACTA TTCCTGATGA TAAACTGAAA CTTTGGATT 1260
GTGGGAACGA ACTGCTTCAG CAGCGGAACA TAAGAAGGAA ACTTCTAACG GAAGTAGATT 1320
TTAATAAAAG TGATGCCAGT CTTCTGGCT CATTGTGGAG ATACAGGCCT GATTCACTTG 1380
ATGGCCCTAT GGAGGGTGAT TCCTGCCCTA CAGGGATTTC TATGAAGGAG TTAAATTTT 1440
CACACCTTCC CTCAAATTCT GTTTCTCCTG GGGACTGTTT ACTGACTACC ACCCTAGGAA 1500
AGACAGGATT CTCTGCCACC AGGAAGAAC CTTTGAAAG GCCTTTATTC AATACCCATT 1560
TACAGAAGTC CTTTGTAAAGT AGCAACTGGG CTGAAACACC AAGACTAGGA AAAAAAAATG 1620
AAAGCTCTTA TTTCCCAGGA AATGTTCTCA CAAGCACTGC TGTGAAAGAT CAGAATAAAC 1680
ATACTGCTTC AATAAATGAC TTAGAAAGAG AAACCCAACC TTCTATGAT ATTGATAATT 1740
TTGACATAGA TGACTTTGAT GATGATGATG ACTGGGAAGA CATAATGCAT AATTAGCAG 1800
CCAGCAAATC TTCCACAGCT GCCTATCAAC CCATCAAGGA AGGTCGGCCA ATTAAATCAG 1860
TATCAGAAAG ACTTTCTCA GCCAAGACAG ACTGTCTTCC AGTGTCTACT ACTGCTAAA 1920
ATATAAAACTT CTCAGAGTCA ATTCAAGATT ATACTGACAA GTCAGCACAA AATTAGCAT 1980
CCAGAAATCT GAAACATGAG CGTTTCCAAA GTCTTAGTTT TCCTCATACA AAGGAAATGA 2040
TGAAGATTTT TCATAAAAAA TTTGGCCTGC ATAATTTAG AACTAATCAG CTAGAGGCGA 2100
TCAATGCTGC ACTGCTTGGT GAAGACTGTT TTATCCTGAT GCCGACTGGA GGTGGTAAGA 2160
GTTTGTGTTA CCAGCTCCCT GCCTGTGTTT CTCCTGGGGT CACTGTTGTC ATTTCTCCCT 2220
TGAGATCACT TATCGTAGAT CAAGTCCAAA AGCTGACTTC CTTGGATATT CCAGCTACAT 2280
ATCTGACAGG TGATAAGACT GACTCAGAAG CTACAAATAT TTACCTCCAG TTATCAAAAA 2340
AAGACCCAAT CATAAAACTT CTATATGTCA CTCCAGAAAA GATCTGTGCA AGTAACAGAC 2400
TCATTTCTAC TCTGGAGAAT CTCTATGAGA GGAAGCTCTT GGCACGTTT GTTATTGATG 2460

AAGCACATTG TGTCAGTCAG TGGGGACATG ATTTTCGTCA AGATTACAAA AGAATGAATA 2520
TGCTTCGCCA GAAGTTTCCT TCTGTTCCGG TGATGGCTCT TACGGCCACA GCTAATCCCA 2580
GGGTACAGAA GGACATCCTG ACTCAGCTGA AGATTCTCAG ACCTCAGGTG TTTAGCATGA 2640
GCTTTAACAG ACATAATCTG AAATACTATG TATTACCGAA AAAGCCTAAA AAGGTGGCAT 2700
TTGATTGCCT AGAATGGATC AGAAAGCACC ACCCATATGA TTCAGGGATA ATTTACTGCC 2760
TCTCCAGGCG AGAATGTGAC ACCATGGCTG ACACGTTACA GAGAGATGGG CTCGCTGCTC 2820
TTGCTTACCA TGCTGGCCTC AGTGATTCTG CCAGAGATGA AGTGCAGCAG AAGTGGATTA 2880
ATCAGGATGG CTGTCAGGTT ATCTGTGCTA CAATTGCATT TGGAAATGGGG ATTGACAAAC 2940
CGGACGTGCG ATTTGTGATT CATGCATCTC TCCCTAAATC TGTGGAGGGT TACTACCAAG 3000
AATCTGGCAG AGCTGGAAGA GATGGGGAAA TATCTCACTG CCTGCTTTTC TATAACCTATC 3060
ATGATGTGAC CAGACTGAAA AGACTTATAA TGATGGAAAA AGATGGAAAC CATCATACAA 3120
GAGAAACTCA CTTCAATAAT TTGTATAGCA TGGTACATTA CTGTGAAAAT ATAACGGAAT 3180
GCAGGAGAAT ACAGCTTTG GCCTACTTTG GTGAAAATGG ATTTAACCT GATTTTGTA 3240
AGAAACACCC AGATGTTCT TGTGATAATT GCTGTAAAAC AAAGGATTAT AAAACAAGAG 3300
ATGTGACTGA CGATGTGAAA AGTATTGTA GATTGTTCA AGAACATAGT TCATCACAAG 3360
GAATGAGAAA TATAAAACAT GTAGGTCCTT CTGGAAGATT TACTATGAAT ATGCTGGTCG 3420
ACATTTCTT GGGGAGTAAG AGTGCACAAA TCCAGTCAGG TATATTTGGA AAAGGATCTG 3480
CTTATTCAAG ACACAATGCC GAAAGACTTT TTAAAAAGCT GATACTTGAC AAGATTTGG 3540
ATGAAGACTT ATATATCAAT GCCAATGACC AGGCGATCGC TTATGTGATG CTCGGAAATA 3600
AAGCCCCAAC TGTACTAAAT GGCAATTAA AGGTAGACTT TATGGAAACA GAAAATTCCA 3660
GCAGTGTGAA AAAACAAAAA GCGTTAGTAG CAAAAGTGTG TCAGAGGGAA GAGATGGTTA 3720
AAAAATGTCT TGGAGAACTT ACAGAAAGTCT GCAAATCTCT GGGGAAAGTT TTTGGTGTCC 3780
ATTACTTCAA TATTTTAAT ACCGTCACTC TCAAGAAGCT TGCAGAAATCT TTATCTTCTG 3840
ATCCTGAGGT TTTGCTTCAA ATTGATGGTG TTACTGAAGA CAAACTGGAA AAATATGGTG 3900
CGGAAGTGAT TTCAGTATTA CAGAAATACT CTGAATGGAC ATGCCAGCT GAAGACAGTT 3960
CCCCAGGGAT AAGCCTGTCC AGCAGCAGAG GCCCCGGAAG AAGTGCCGCT GAGGAGCTTG 4020

ACGAGGAAAT ACCCGTATCT TCCCCTACT TTGCAAGTAA AACCGAGAAAT GAAAGGAAGA 4080
GGAAAAAGAT GCCAGCCTCC CAAAGGTCTA AGAGGAGAAA AACTGCTTCC AGTGGTTCCA 4140
AGGCAAAGGG GGGGTCTGCC ACATGTAGAA AGATATCTTC CAAAACGAAA TCCTCCAGCA 4200
TCATTGGATC CAGTTCAGCC TCACATACTT CTCAAGCGAC ATCAGGAGCC AATAGCAAAT 4260
TGGGGATTAT GGCTCCACCG AAGCCTATAA ATAGACCGTT TCTTAAGCCT TCATATGCAT 4320
TCTCATAACA ACCGAATCTC AATGTACATA GACCCTCTT CTTGTTGTC AGCATCTGAC 4380
CATCTGTGAC TATAAAGCTG TTATTCTTGT TATACCAAAA AAAAAAAA AAAAAAA 4437

(74) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

GCTTCCGGCG GAAGTGAGCC AGGGCTTGGC GC GGCGGCG TG GTTGCGGC 50
GCGGGAAGTT TGGAT 65

(75) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:
(A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

Phe Pro His Thr Lys Glu Met Met Lys Ile Phe His Lys Lys Phe
1 5 10 15

Gly Leu His Asn Phe Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala
20 25 30

Ala Leu Leu Gly Glu Asp Cys Phe Ile Leu Met Pro Thr Gly Gly
35 40 45

Gly Lys Ser Leu Cys Tyr Gln Leu Pro Ala Cys Val Ser Pro Gly
50 55 60

Val Thr Val Val Ile Ser Pro Leu Arg Ser Leu Ile Val Asp Gln
65 70 75

Val Gln Lys Leu Thr Ser Leu Asp Ile Pro Ala Thr Tyr Leu Thr
80 85 90

Gly Asp Lys Thr Asp Ser Glu Ala Thr Asn Ile Tyr Leu Gln Leu
95 100 105

Ser Lys Lys Asp Pro Ile Ile Lys Leu Leu Tyr Val Thr Pro Glu
110 115 120

Lys Ile Cys Ala Ser Asn Arg Leu Ile Ser Thr Leu Glu Asn Leu
125 130 135

Tyr Glu-Arg Lys Leu Leu Ala Arg Phe Val Ile Asp Glu Ala His
140 145 150

Cys Val Ser Gln Trp Gly His Asp Phe Arg Gln Asp Tyr Lys Arg
155 160 165

Met Asn Met Leu Arg Gln Lys Phe Pro Ser Val Pro Val Met Ala
170 175 180

Leu Thr Ala Thr Ala Asn Pro Arg Val Gln Lys Asp Ile Leu Thr
185 190 195

Gln Leu Lys Ile Leu Arg Pro Gln Val Phe Ser Met Ser Phe Asn
200 205 210

Arg His Asn Leu Lys Tyr Tyr Val Leu Pro Lys Lys Pro Lys Lys
215 220 225

Val Ala Phe Asp Cys Leu Glu Trp Ile Arg Lys His His Pro Tyr
230 235 240

Asp Ser Gly Ile Ile Tyr Cys Leu Ser Arg Arg Glu Cys Asp Thr
245 250 255

Met Ala Asp Thr Leu Gln Arg Asp Gly Leu Ala Ala Leu Ala Tyr
260 265 270

His Ala Gly Leu Ser Asp Ser Ala Arg Asp Glu Val Gln Gln Lys
275 280 285

Trp Ile Asn Gln Asp Gly Cys Gln Val Ile Cys Ala Thr Ile Ala
290 295 300

Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Ile His
305 310 315

Ala Ser Leu Pro Lys Ser Val Glu Gly Tyr Tyr Gln Glu Ser Gly
320 325 330

Arg Ala Gly Arg Asp Gly Glu Ile Ser His Cys Leu Leu Phe Tyr
335 340 345

Thr Tyr His Asp Val Thr Arg Leu Lys Arg Leu Ile Met Met Glu
350 355 360

Lys Asp Gly Asn His His Thr Arg Glu Thr His Phe Asn Asn Leu
365 370 375

Tyr Ser Met Val His Tyr Cys Glu Asn Ile Thr Glu Cys Arg Arg
380 385 390

Ile Gln Leu

(76) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:
(A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

Phe Pro Trp Ser Gly Lys Val Lys Asp Ile Leu Gln Asn Val Phe
1 5 10 15

Lys Leu Glu Lys Phe Arg Pro Leu Gln Leu Glu Thr Ile Asn Val
20 25 30

Thr Met Ala Gly Lys Glu Val Phe Leu Val Met Pro Thr Gly Gly
35 40 45

Gly Lys Ser Leu Cys Tyr Gln Leu Pro Ala Leu Cys Ser Asp Gly
50 55 60

Phe Thr Leu Val Ile Cys Pro Leu Ile Ser Leu Met Glu Asp Gln
65 70 75

Leu Met Val Leu Lys Gln Leu Gly Ile Ser Ala Thr Met Leu Asn
80 85 90

Ala Ser Ser Ser Lys Glu His Val Lys Trp Val His Asp Glu Met
95 100 105

Val Asn Lys Asn Ser Glu Leu Lys Leu Ile Tyr Val Thr Pro Glu
110 115 120

Lys Ile Ala Lys Ser Lys Met Phe Met Ser Arg Leu Glu Lys Ala
125 130 135

Tyr Glu Ala Arg Arg Phe Thr Arg Ile Ala Val Asp Glu Val His
140 145 150

Cys Cys Ser Gln Trp Gly His Asp Phe Arg Pro Asp Tyr Lys Ala
155 160 165

Leu Gly Ile Leu Lys Arg Gln Phe Pro Asn Ala Ser Leu Ile Gly
170 175 180

Leu Thr Ala Thr Ala Thr Asn His Val Leu Thr Asp Ala Gln Lys
185 190 195

Ile Leu Cys Ile Glu Lys Cys Phe Thr Phe Thr Ala Ser Phe Asn
200 205 210

Arg Pro Asn Leu Tyr Tyr Glu Val Arg Gln Lys Pro Ser Asn Thr
215 220 225

Glu Asp Phe Ile Glu Asp Ile Val Lys Leu Ile Asn Gly Arg Tyr
230 235 240

Lys Gly Gln Ser Gly Ile Ile Tyr Cys Phe Ser Gln Lys Asp Ser
245 250 255

Glu Gln Val Thr Val Ser Leu Gln Asn Leu Gly Ile His Ala Gly
260 265 270

Ala Tyr His Ala Asn Leu Glu Pro Glu Asp Lys Thr Thr Val His
275 280 285

Arg Lys Trp Ser Ala Asn Glu Ile Gln Val Val Val Ala Thr Val
290 295 300

Ala Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Ile
305 310 315

His His Ser Met Ser Lys Ser Met Glu Asn Tyr Tyr Gln Glu Ser
320 325 330

Gly Arg Ala Gly Arg Asp Asp Met Lys Ala Asp Cys Ile Leu Tyr
335 340 345

Tyr Gly Phe Gly Asp Ile Phe Arg Ile Ser Ser Met Val Val Met
350 355 360

Glu Asn Val Gly Gln Gln Lys Leu Tyr Glu Met Val Ser Tyr Cys
365 370 375

Gln Asn Ile Ser Lys Ser Arg Arg Val Leu Met
380 385

(77) INFORMATION FOR SEQ ID NO: 76

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

Tyr	Pro	Trp	Ser	Asp	Glu	Val	Leu	Tyr	Arg	Leu	His	Glu	Val	Phe
1				5					10					15
Lys	Leu	Pro	Gly	Phe	Arg	Pro	Asn	Gln	Leu	Glu	Ala	Val	Asn	Ala
				20					25					30
Thr	Leu	Gln	Gly	Lys	Asp	Val	Phe	Val	Leu	Met	Pro	Thr	Gly	Gly
				35					40					45
Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Val	Val	Lys	Ser	Gly
				50					55					60
Lys	Thr	His	Gly	Thr	Thr	Ile	Val	Ile	Ser	Pro	Leu	Ile	Ser	Leu
				65					70					75
Met	Gln	Asp	Gln	Val	Glu	His	Leu	Leu	Asn	Lys	Asn	Ile	Lys	Ala
				80					85					90
Ser	Met	Phe	Ser	Ser	Arg	Gly	Thr	Ala	Glu	Gln	Arg	Arg	Gln	Thr
				95					100					105
Phe	Asn	Leu	Phe	Ile	Asn	Gly	Leu	Leu	Asp	Leu	Val	Tyr	Ile	Ser
				110					115					120
Pro	Glu	Met	Ile	Ser	Ala	Ser	Glu	Gln	Cys	Lys	Arg	Ala	Ile	Ser
				125					130					135
Arg	Leu	Tyr	Ala	Asp	Gly	Lys	Leu	Ala	Arg	Ile	Val	Val	Asp	Glu
				140					145					150
Ala	His	Cys	Val	Ser	Asn	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr
				155					160					165
Lys	Glu	Leu	Lys	Phe	Phe	Lys	Arg	Glu	Tyr	Pro	Asp	Ile	Pro	Met
				170					175					180
Ile	Ala	Leu	Thr	Ala	Thr	Ala	Ser	Glu	Gln	Val	Arg	Met	Asp	Ile
				185					190					195

Ile His Asn Leu Glu Leu Lys Glu Pro Val Phe Leu Lys Gln Ser
200 205 210

Phe Asn Arg Thr Asn Leu Tyr Tyr Glu Val Asn Lys Lys Thr Lys
215 220 225

Asn Thr Ile Phe Glu Ile Cys Asp Ala Val Lys Ser Arg Phe Lys
230 235 240

Asn Gln Thr Gly Ile Ile Tyr Cys His Ser Lys Lys Ser Cys Glu
245 250 255

Gln Thr Ser Ala Gln Met Gln Arg Asn Gly Ile Lys Cys Ala Tyr
260 265 270

Tyr His Ala Gly Met Glu Pro Asp Glu Arg Leu Ser Val Gln Lys
275 280 285

Ala Trp Gln Ala Asp Glu Ile Gln Val Ile Cys Ala Thr Val Ala
290 295 300

Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Tyr His
305 310 315

Phe Thr Val Pro Arg Thr Leu Glu Gly Tyr Tyr Gln Glu Thr Gly
320 325 330

Arg Ala Gly Arg Asp Gly Asp Tyr Ser Tyr Cys Ile Thr Tyr Phe
335 340 345

Ser Phe Arg Asp Ile Arg Thr Met Gln Thr Met Ile Gln Lys Asp
350 355 360

Lys Asn Leu Asp Arg Glu Asn Lys Glu Lys His Leu Asn Lys Leu
365 370 375

Gln Gln Val Met Ala Tyr Cys Asp Asn Val Thr Asp Cys Arg Arg
380 385 390

Lys Leu Val

(78) INFORMATION FOR SEQ ID NO: 77

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:
- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

Val Leu Gln Glu Thr Phe Gly Tyr Gln Gln Phe Arg Pro Gly Gln
1 5 10 15

Glu Glu Ile Ile Asp Thr Val Leu Ser Gly Arg Asp Cys Leu Val
20 25 30

Val Met Pro Thr Gly Gly Lys Ser Leu Cys Tyr Gln Ile Pro
35 40 45

Ala Leu Leu Leu Asn Gly Leu Thr Val Val Val Ser Pro Leu Ile
50 55 60

Ser Leu Met Lys Asp Gln Val Asp Gln Leu Gln Ala Asn Gly Val
65 70 75

Ala Ala Ala Cys Leu Asn Ser Thr Gln Thr Arg Glu Gln Gln Leu
80 85 90

Glu Val Met Thr Gly Cys Arg Thr Gly Gln Ile Arg Leu Leu Tyr
95 100 105

Ile Ala Pro Glu Arg Leu Met Leu Asp Asn Phe Leu Glu His Leu
110 115 120

Ala His Trp Asn Pro Val Leu Leu Ala Val Asp Glu Ala His Cys
125 130 135

Ile Ser Gln Trp Gly His Asp Phe Arg Pro Glu Tyr Ala Ala Leu
140 145 150

Gly Gln Leu Arg Gln Arg Phe Pro Thr Leu Pro Phe Met Ala Leu
155 160 165

Thr Ala Thr Ala Asp Asp Thr Thr Arg Gln Asp Ile Val Arg Leu
170 175 180

Leu Gly Leu Asn Asp Pro Leu Ile Gln Ile Ser Ser Phe Asp Arg
185 190 195

Pro Asn Ile Arg Tyr Met Leu Met Glu Lys Phe Lys Pro Leu Asp

200	205	210
Gln Leu Met Arg Tyr Val Gln Glu Gln Arg Gly Lys Ser Gly Ile		
215	220	225
Ile Tyr Cys Asn Ser Arg Ala Lys Val Glu Asp Thr Ala Ala Ala		
230	235	240
Leu Gln Ser Lys Gly Ile Ser Ala Ala Ala Tyr His Ala Gly Leu		
245	250	255
Glu Asn Asn Val Arg Ala Asp Val Gln Glu Lys Phe Gln Arg Asp		
260	265	270
Asp Leu Gln Ile Val Val Ala Thr Val Ala Phe Gly Met Gly Ile		
275	280	285
Asn Lys Pro Asn Val Arg Phe Val Val His Phe Asp Ile Pro Arg		
290	295	300
Asn Ile Glu Ser Tyr Tyr Gln Glu Thr Gly Arg Ala Gly Arg Asp		
305	310	315
Gly Leu Pro Ala Glu Ala Met Leu Phe Tyr Asp Pro Ala Asp Met		
320	325	330
Ala Trp Leu Arg Arg Cys Leu Glu Glu Lys Pro Gln Gly Gln Leu		
335	340	345
Gln Asp Ile Glu Arg His Lys Leu Asn Ala Met Gly Ala Phe Ala		
350	355	360
Glu Ala Gln Thr Cys Arg Arg Leu Val Leu		
365	370	

(79) INFORMATION FOR SEQ ID NO: 78

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1417
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

Met	Ala	Ala	Val	Pro	Gln	Asn	Asn	Leu	Gln	Glu	Gln				
1					5				10						
Leu	Glu	Arg	His	Ser	Ala	Arg	Thr	Leu	Asn	Asn	Lys	Leu	Ser	Leu	Ser
	15					20					25				
Lys	Pro	Lys	Phe	Ser	Gly	Phe	Thr	Phe	Lys	Lys	Lys	Thr	Ser	Ser	Asp
	30				35				40						
Asn	Asn	Val	Ser	Val	Thr	Asn	Val	Ser	Val	Ala	Lys	Thr	Pro	Val	Leu
	45				50				55		60				
Arg	Asn	Lys	Asp	Val	Asn	Val	Thr	Glu	Asp	Phe	Ser	Phe	Ser	Glu	Pro
	65					70				75					
Leu	Pro	Asn	Thr	Thr	Asn	Gln	Gln	Arg	Val	Lys	Asp	Phe	Phe	Lys	Asn
	80					85				90					
Ala	Pro	Ala	Gly	Gln	Glu	Thr	Gln	Arg	Gly	Gly	Ser	Lys	Ser	Leu	Leu
	95					100				105					
Pro	Asp	Phe	Leu	Gln	Thr	Pro	Lys	Glu	Val	Val	Cys	Thr	Thr	Gln	Asn
	110					115				120					
Thr	Pro	Thr	Val	Lys	Lys	Ser	Arg	Asp	Thr	Ala	Leu	Lys	Lys	Leu	Glu
	125				130					135		140			
Phe	Ser	Ser	Ser	Pro	Asp	Ser	Leu	Ser	Thr	Ile	Asn	Asp	Trp	Asp	Asp
	145					150				155					
Met	Asp	Asp	Phe	Asp	Thr	Ser	Glu	Thr	Ser	Lys	Ser	Phe	Val	Thr	Pro
	160					165				170					
Pro	Gln	Ser	His	Phe	Val	Arg	Val	Ser	Thr	Ala	Gln	Lys	Ser	Lys	Lys
	175					180				185					
Gly	Lys	Arg	Asn	Phe	Phe	Lys	Ala	Gln	Leu	Tyr	Thr	Thr	Asn	Thr	Val
	190					195				200					
Lys	Thr	Asp	Leu	Pro	Pro	Pro	Ser	Ser	Glu	Ser	Glu	Gln	Ile	Asp	Leu
	205					210				215		220			

Thr Glu Glu Gln Lys Asp Asp Ser Glu Trp Leu Ser Ser Asp Val Ile
225 230 235

Cys Ile Asp Asp Gly Pro Ile Ala Glu Val His Ile Asn Glu Asp Ala
240 245 250

Gln Glu Ser Asp Ser Leu Lys Thr His Leu Glu Asp Glu Arg Asp Asn
255 260 265

Ser Glu Lys Lys Asn Leu Glu Glu Ala Glu Leu His Ser Thr Glu
270 275 280

Lys Val Pro Cys Ile Glu Phe Asp Asp Asp Tyr Asp Thr Asp Phe
285 290 295 300

Val Pro Pro Ser Pro Glu Glu Ile Ile Ser Ala Ser Ser Ser Ser
305 310 315

Lys Cys Leu Ser Thr Leu Lys Asp Leu Asp Thr Ser Asp Arg Lys Glu
320 325 330

Asp Val Leu Ser Thr Ser Lys Asp Leu Leu Ser Lys Pro Glu Lys Met
335 340 345

Ser Met Gln Glu Leu Asn Pro Glu Thr Ser Thr Asp Cys Asp Ala Arg
350 355 360

Gln Ile Ser Leu Gln Gln Leu Ile His Val Met Glu His Ile Cys
365 370 375 380

Lys Leu Ile Asp Thr Ile Pro Asp Asp Lys Leu Lys Leu Asp Cys
385 390 395

Gly Asn Glu Leu Leu Gln Gln Arg Asn Ile Arg Arg Lys Leu Leu Thr
400 405 410

Glu Val Asp Phe Asn Lys Ser Asp Ala Ser Leu Leu Gly Ser Leu Trp
415 420 425

Arg Tyr Arg Pro Asp Ser Leu Asp Gly Pro Met Glu Gly Asp Ser Cys
430 435 440

Pro Thr Gly Asn Ser Met Lys Glu Leu Asn Phe Ser His Leu Pro Ser
445 450 455 460

Asn Ser Val Ser Pro Gly Asp Cys Leu Leu Thr Thr Thr Leu Gly Lys
465 470 475

Thr Gly Phe Ser Ala Thr Arg Lys Asn Leu Phe Glu Arg Pro Leu Phe
480 485 490

Asn Thr His Leu Gln Lys Ser Phe Val Ser Ser Asn Trp Ala Glu Thr

495	500	505
Pro Arg Leu Gly Lys Lys Asn Glu Ser Ser Tyr Phe Pro Gly Asn Val		
510	515	520
Leu Thr Ser Thr Ala Val Lys Asp Gln Asn Lys His Thr Ala Ser Ile		
525	530	535
		540
Asn Asp Leu Glu Arg Glu Thr Gln Pro Ser Tyr Asp Ile Asp Asn Phe		
545	550	555
Asp Ile Asp Asp Phe Asp Asp Asp Asp Trp Glu Asp Ile Met His		
560	565	570
Asn Leu Ala Ala Ser Lys Ser Ser Thr Ala Ala Tyr Gln Pro Ile Lys		
575	580	585
Glu Gly Arg Pro Ile Lys Ser Val Ser Glu Arg Leu Ser Ser Ala Lys		
590	595	600
Thr Asp Cys Leu Pro Val Ser Ser Thr Ala Gln Asn Ile Asn Phe Ser		
605	610	615
		620
Glu Ser Ile Gln Asn Tyr Thr Asp Lys Ser Ala Gln Asn Leu Ala Ser		
625	630	635
Arg Asn Leu Lys His Glu Arg Phe Gln Ser Leu Ser Phe Pro His Thr		
640	645	650
Lys Glu Met Met Lys Ile Phe His Lys Lys Phe Gly Leu His Asn Phe		
655	660	665
Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala Ala Leu Leu Gly Glu Asp		
670	675	680
Cys Phe Ile Leu Met Pro Thr Gly Gly Lys Ser Leu Cys Tyr Gln		
685	690	695
		700
Leu Pro Ala Cys Val Ser Pro Gly Val Thr Val Val Ile Ser Pro Leu		
705	710	715
Arg Ser Leu Ile Val Asp Gln Val Gln Lys Leu Thr Ser Leu Asp Ile		
720	725	730
Pro Ala Thr Tyr Leu Thr Gly Asp Lys Thr Asp Ser Glu Ala Thr Asn		
735	740	745
Ile Tyr Leu Gln Leu Ser Lys Lys Asp Pro Ile Ile Lys Leu Leu Tyr		
750	755	760
Val Thr Pro Glu Lys Ile Cys Ala Ser Asn Arg Leu Ile Ser Thr Leu		
765	770	775
		780

Glu Asn Leu Tyr Glu Arg Lys Leu Leu Ala Arg Phe Val Ile Asp Glu
785 790 795

Ala His Cys Val Ser Gln Trp Gly His Asp Phe Arg Gln Asp Tyr Lys
800 805 810

Arg Met Asn Met Leu Arg Gln Lys Phe Pro Ser Val Pro Val Met Ala
815 820 825

Leu Thr Ala Thr Ala Asn Pro Arg Val Gln Lys Asp Ile Leu Thr Gln
830 835 840

Leu Lys Ile Leu Arg Pro Gln Val Phe Ser Met Ser Phe Asn Arg His
845 850 855 860

Asn Leu Lys Tyr Tyr Val Leu Pro Lys Lys Pro Lys Lys Val Ala Phe
865 870 875

Asp Cys Leu Glu Trp Ile Arg Lys His His Pro Tyr Asp Ser Gly Ile
880 885 890

Ile Tyr Cys Leu Ser Arg Arg Glu Cys Asp Thr Met Ala Asp Thr Leu
895 900 905

Gln Arg Asp Gly Leu Ala Ala Leu Ala Tyr His Ala Gly Leu Ser Asp
910 915 920

Ser Ala Arg Asp Glu Val Gln Gln Lys Trp Ile Asn Gln Asp Gly Cys
925 930 935 940

Gln Val Ile Cys Ala Thr Ile Ala Phe Gly Met Gly Ile Asp Lys Pro
945 950 955

Asp Val Arg Phe Val Ile His Ala Ser Leu Pro Lys Ser Val Glu Gly
960 965 970

Tyr Tyr Gln Glu Ser Gly Arg Ala Gly Arg Asp Gly Glu Ile Ser His
975 980 985

Cys Leu Leu Phe Tyr Thr Tyr His Asp Val Thr Arg Leu Lys Arg Leu
990 995 1000

Ile Met Met Glu Lys Asp Gly Asn His His Thr Arg Glu Thr His Phe
1005 1010 1015 1020

Asn Asn Leu Tyr Ser Met Val His Tyr Cys Glu Asn Ile Thr Glu Cys
1025 1030 1035

Arg Arg Ile Gln Leu Leu Ala Tyr Phe Gly Glu Asn Gly Phe Asn Pro
1040 1045 1050

Asp Phe Cys Lys Lys His Pro Asp Val Ser Cys Asp Asn Cys Cys Lys
1055 1060 1065

Thr Lys Asp Tyr Lys Thr Arg Asp Val Thr Asp Asp Val Lys Ser Ile
1070 1075 1080

Val Arg Phe Val Gln Glu His Ser Ser Ser Gln Gly Met Arg Asn Ile
1085 1090 1095 1100

Lys His Val Gly Pro Ser Gly Arg Phe Thr Met Asn Met Leu Val Asp
1105 1110 1115

Ile Phe Leu Gly Ser Lys Ser Ala Lys Ile Gln Ser Gly Ile Phe Gly
1120 1125 1130

Lys Gly Ser Ala Tyr Ser Arg His Asn Ala Glu Arg Leu Phe Lys Lys
1135 1140 1145

Leu Ile Leu Asp Lys Ile Leu Asp Glu Asp Leu Tyr Ile Asn Ala Asn
1150 1155 1160

Asp Gln Ala Ile Ala Tyr Val Met Leu Gly Asn Lys Ala Gln Thr Val
1165 1170 1175 1180

Leu Asn Gly Asn Leu Lys Val Asp Phe Met Glu Thr Glu Asn Ser Ser
1185 1190 1195

Ser Val Lys Lys Gln Lys Ala Leu Val Ala Lys Val Ser Gln Arg Glu
1200 1205 1210

Glu Met Val Lys Lys Cys Leu Gly Glu Leu Thr Glu Val Cys Lys Ser
1215 1220 1225

Leu Gly Lys Val Phe Gly Val His Tyr Phe Asn Ile Phe Asn Thr Val
1230 1235 1240

Thr Leu Lys Lys Leu Ala Glu Ser Leu Ser Ser Asp Phe Glu Val Leu
1245 1250 1255 1260

Leu Gln Ile Asp Gly Val Thr Glu Asp Lys Leu Glu Lys Tyr Gly Ala
1265 1270 1275

Glu Val Ile Ser Val Leu Gln Lys Tyr Ser Glu Trp Thr Ser Pro Ala
1280 1285 1290

Glu Asp Ser Ser Pro Gly Ile Ser Leu Ser Ser Arg Gly Pro Gly
1295 1300 1305

Arg Ser Ala Ala Glu Glu Leu Asp Glu Glu Ile Pro Val Ser Ser His
1310 1315 1320

Tyr Phe Ala Ser Lys Thr Arg Asn Glu Arg Lys Arg Lys Lys Met Pro
1325 1330 1335 1340
Ala Ser Gln Arg Ser Lys Arg Arg Lys Thr Ala Ser Ser Gly Ser Lys
1345 1350 1355
Ala Lys Gly Gly Ser Ala Thr Cys Arg Lys Ile Ser Ser Lys Thr Lys
1360 1365 1370
Ser Ser Ser Ile Ile Gly Ser Ser Ala Ser His Thr Ser Gln Ala
1375 1380 1385
Thr Ser Gly Ala Asn Ser Lys Leu Gly Ile Met Ala Pro Pro Lys Pro
1390 1395 1400
Ile Asn Arg Pro Phe Leu Lys Pro Ser Tyr Ala Phe Ser
1405 1410 1415